RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/763,129A

Source: PCT09

Date Processed by STIC: 4\9\02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
                Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/763,129A |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
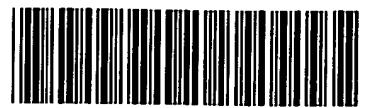<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

Does Not Comply   PCT09
Corrected Diskette Needed

Errors on pp. 3-5

RAW SEQUENCE LISTING   DATE: 04/09/2002
PATENT APPLICATION: US/09/763,129A   TIME: 12:29:23

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04092002\I763129A.raw**

```
 3 <110> APPLICANT: CO, MAN SUNG
 4         MAXIMILLIANO, VASQUEZ
 6 <120> TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
FACTOR MONOCLONAL
 7         ANTIBODY
 9 <130> FILE REFERENCE: 202617US0PCT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/763,129A
C--> 12 <141> CURRENT FILING DATE: 2001-05-16
14 <150> PRIOR APPLICATION NUMBER: PCT/US99/16724
15 <151> PRIOR FILING DATE: 1999-08-19
17 <150> PRIOR APPLICATION NUMBER: 09/136,315
18 <151> PRIOR FILING DATE: 1998-08-19
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 417
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(417)
32 <223> OTHER INFORMATION:
35 <400> SEQUENCE: 1
36 atg gat ttt ggg ctg att ttt ttt att gtt gct ctt tta aaa ggg gtc      48
37 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
38 1               5                   10                  15
40 cag tgt gag gtg aaa ctt ctc gag tct gga ggt ggc ctg gtg cag act      96
41 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr
42             20                  25                  30
44 gga gga tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt     144
45 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
46         35                  40                  45
48 aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa     192
49 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50     50                  55                  60
52 tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca     240
53 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
54 65                  70                  75                  80
56 tct cta aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg     288
57 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
58                 85                  90                  95
60 ctg tac ctg caa atg agt caa gtg aga tct gag gac aca gcc ctt tac     336
61 Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr
62             100                 105                 110
```

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 64 tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac       384
 65 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
 66         115                 120                 125
 68 tgg ggc caa ggg act ctg gtc tct gtc tcg cca                           417
 69 Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro
 70         130                 135
 73 <210> SEQ ID NO: 2
 74 <211> LENGTH: 139
 75 <212> TYPE: PRT
 76 <213> ORGANISM: Mus musculus
 78 <400> SEQUENCE: 2
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 81 1               5                   10                  15
 84 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr
 85             20                  25                  30
 88 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
 89         35                  40      r       45
 92 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 93     50                  55                  60
 96 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
 97 65                  70                  75                  80
100 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
101             85                  90                  95
104 Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr
105             100                 105                 110
108 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
109         115                 120                 125
112 Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro
113         130                 135
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 381
118 <212> TYPE: DNA
119 <213> ORGANISM: Mus musculus
121 <220> FEATURE:
122 <221> NAME/KEY: CDS
123 <222> LOCATION: (1)..(381)
124 <223> OTHER INFORMATION:
127 <400> SEQUENCE: 3
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130 1               5                   10                  15
132 gat gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct        96
133 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
134             20                  25                  30
136 gta tct gtg gga gaa act gtc acc atc aca tgt cga gca agt gag aat       144
137 Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
138         35                  40                  45
140 att tac aat aat tta gct tgg tat cag cag aga cag gga aaa tct cct       192
141 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro
```

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142      50                   55                   60
144 cag ctc ctg gtc tat gct gca aca aac tta gca gat ggt gtg cca tca      240
145 Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
146 65                   70                   75                   80
148 agg ttc agt ggc agt gga tca ggc aca cag tat tcc ctc aag atc gac      288
149 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
150                  85                   90                   95
152 agc ctg cag tct gaa gat ttt ggg agt tat tac tgt caa cat ttg tgg      336
153 Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
154                  100                  105                  110
156 act tct ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa          381
157 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
158         115                  120                  125
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 127
163 <212> TYPE: PRT
164 <213> ORGANISM: Mus musculus
166 <400> SEQUENCE: 4
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172 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
173             20                  25                  30
176 Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
177         35                  40                  45
180 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro
181      50                  55                  60
184 Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
185 65                  70                  75                  80
188 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
189                  85                  90                  95
192 Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
193             100                  105                  110
196 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
197         115                  120                  125
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 417
202 <212> TYPE: DNA
203 <213> ORGANISM: hybrid
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (1)..(417)
208 <223> OTHER INFORMATION:
211 <400> SEQUENCE: 5
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213 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
214 1             5                   10                  15
216 cag tgt gag gtg caa ctt gtc gag tct gga ggt gga cta gtg cag cct      96
217 Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
218             20                  25                  30
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(handwritten annotation pointing to line 203 "hybrid": — invalid response, see error summary sheet item 10)

RAW SEQUENCE LISTING   DATE: 04/09/2002
PATENT APPLICATION: US/09/763,129A   TIME: 12:29:23

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Output Set: N:\CRF3\04092002\I763129A.raw

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220 gga gga tca ctg aga ctc tcc tgt gca gcc tca gga ttc gat ttt agt   144
221 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
222         35              40               45
224 aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg ctc gag   192
225 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
226     50              55               60
228 tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca   240
229 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
230 65              70              75               80
232 tct cta aag gat aaa ttc acc atc tcc aga gac aac gcc aaa aat acg   288
233 Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
234             85              90              95
236 ctg tac ctg caa atg aac tca ttg aga gct gag gac acg gcc gtt tac   336
237 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
238         100             105             110
240 tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac   384
241 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
242         115             120             125
244 tgg ggc caa ggg act ctg gtc acc gtc tcc tca                       417
245 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser                     o
246     130             135
249 <210> SEQ ID NO: 6
250 <211> LENGTH: 139
251 <212> TYPE: PRT
252 <213> ORGANISM: (hybrid)  - same error
254 <400> SEQUENCE: 6
256 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
257 1               5               10              15
260 Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
261         20              25              30
264 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
265         35              40              45
268 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
269     50              55              60
272 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
273 65              70              75              80
276 Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
277             85              90              95
280 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
281         100             105             110
284 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
285         115             120             125
288 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
289     130             135
292 <210> SEQ ID NO: 7
293 <211> LENGTH: 381
294 <212> TYPE: DNA
295 <213> ORGANISM: (hybrid)  - same
297 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 04/09/2002
PATENT APPLICATION: US/09/763,129A   TIME: 12:29:23

Input Set : A:\EP.txt
Output Set: N:\CRF3\04092002\I763129A.raw

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298 <221> NAME/KEY: CDS
299 <222> LOCATION: (1)..(381)
300 <223> OTHER INFORMATION:
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305 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
306 1               5                   10                  15
308 gat gcc aga tgt gac atc cag atg act cag tct cca tcc tcc cta tct       96
309 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
310             20                  25                  30
312 gca tct gtg gga gac agg gtc acc atc aca tgt cga gca agt gag aat      144
313 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
314         35                  40                  45
316 att tac aat aat tta gct tgg tat cag cag aaa ccg gga aaa gct cct      192
317 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
318     50                  55                  60
320 aag cta cta gtc tat gct gca aca aac tta gca gat ggt gtg cca tca      240
321 Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
322 65                  70                  75                  80
324 agg ttc agt ggc agt gga tca ggc aca cag tat acc ctc acg atc agc      288
325 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser
326                 85                  90                  95
328 agc ctc cag cct gag gat ttt gcg act tat tac tgt caa cat ttg tgg      336
329 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp
330             100                 105                 110
332 act tct ccg tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa        381
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334         115                 120                 125
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338 <211> LENGTH: 127
339 <212> TYPE: PRT                    -same
340 <213> ORGANISM: (hybrid)
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348 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
349             20                  25                  30
352 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
353         35                  40                  45
356 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
357     50                  55                  60
360 Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
361 65                  70                  75                  80
364 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser
365                 85                  90                  95
368 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp
369             100                 105                 110
372 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
373         115                 120                 125
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VERIFICATION SUMMARY   DATE: 04/09/2002
PATENT APPLICATION: **US/09/763,129A**   TIME: 12:29:24

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04092002\I763129A.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date